

IN THE CLAIMS

This listing of the claims replaces all prior versions of the claims in the application.

Claims 1-231 (Cancelled)

232. (New) An isolated polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:41,
- b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:41, and
- c) an immunogenic fragment of a polypeptide having the amino acid sequence of SEQ ID NO:41.

233. (New) An isolated polypeptide of claim 232 comprising the amino acid sequence of SEQ ID NO:41.

234. (New) An isolated polypeptide of claim 232 comprising a naturally occurring amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO:41.

235. (New) An isolated polynucleotide encoding a polypeptide of claim 232.

236. (New) An isolated polynucleotide encoding a polypeptide of claim 233.

237. (New) An isolated polynucleotide encoding a polypeptide of claim 234.

238. (New) An isolated polynucleotide of claim 236 comprising the polynucleotide sequence of SEQ ID NO:84.

239. (New) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 235.

240. (New) A cell transformed with a recombinant polynucleotide of claim 239.

241. (New) A method of producing a polypeptide encoded by a polynucleotide of claim 235, the method comprising:

- a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide of claim 235, and
- b) recovering the polypeptide so expressed.

242. (New) An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising the polynucleotide sequence of SEQ ID NO:84,
- b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to the polynucleotide sequence of SEQ ID NO:84,
- c) a polynucleotide complementary to a polynucleotide of a),
- d) a polynucleotide complementary to a polynucleotide of b), and
- e) an RNA equivalent of a)-d).

243. (New) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 242, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

244. (New) A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 242, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

245. (New) A composition comprising a polypeptide of claim 232 and a pharmaceutically acceptable excipient.

246. (New) A composition of claim 245. Where the polypeptide comprises the amino acid sequence of SEQ ID NO:41

247. (New) A method of screening a compound for effectiveness as an agonist of a polypeptide of claim 232, the method comprising:

- a) contacting a sample comprising a polypeptide of claim 232 with a compound, and
- b) detecting agonist activity in the sample.

248. (New) A method of screening a compound for effectiveness as an antagonist of a polypeptide of claim 232, the method comprising:

- a) contacting a sample comprising a polypeptide of claim 232 with a compound, and
- b) detecting antagonist activity in the sample.

249. (New) A method of screening for a compound that modulates the activity of the polypeptide of claim 232, the method comprising:

- a) combining the polypeptide of claim 232 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 232,
- b) assessing the activity of the polypeptide of claim 232 in the presence of the test compound, and
- c) comparing the activity of the polypeptide of claim 232 in the presence of the test compound with the activity of the polypeptide of claim 232 in the absence of the

test compound, wherein a change in the activity of the polypeptide of claim 232 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 232.

250. (New) A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 238, the method comprising:

- a) contacting a sample comprising the target polynucleotide with a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

251. (New) A method of screening for potential toxicity of a test compound, the method comprising:

- a) treating a biological sample containing nucleic acids with the test compound,
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 242 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 242 or fragment thereof,
- c) quantifying the amount of hybridization complex, and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample indicates potential toxicity of the test compound.